

HUMAN xiap

SEQ ID NO:3

1 gaaaggtggacaagtcctaattccaagagaagatgactttaacagtttgaagatct
-----+-----+-----+-----+-----+ 60

SEQ ID NO:4 a

M T F N S F E G S -

61 aaaacttggtacctgcagacatcaataaggaagaagaattttagaagagtttaataga
-----+-----+-----+-----+-----+ 120

a K T C V P A D I N K E E F V E E F N R -

121 ttaaaaacttttgctaatttccaagtggtagtcctgtttcagcatcaacactggcagca
-----+-----+-----+-----+-----+ 180

a L K T F A N F P S G S P V S A S T L A R -

181 gcagggttcttatactggtgaagagataccgtgcggtgttagttgtcatgcagct
-----+-----+-----+-----+-----+ 240

a A G F L Y T G E G D T V R C F S C H A A -

241 gtagatagatggcaatatggagactcagcagttggaagacacaggaagtatccccaat
-----+-----+-----+-----+-----+ 300

a V D R W Q Y G D S A V G R H R K V S P N -

301 tgcagattatcaacggcttttatcttgaataatagtgccacgcagtcctacaattctggt
-----+-----+-----+-----+-----+ 360

a C R F I N G F Y L E N S A T Q S T N S G -

Fig. 1 (page 1 of 7)



HUMAN xiap

```

a      361  atccagaatggtcagtacaaagttgaaaactatctgggaagcagagatcatttgcctta
      -----+-----+-----+-----+-----+-----+ 420
a      I  Q  N  G  Q  Y  K  V  E  N  Y  L  G  S  R  D  H  F  A  L  -
      421  gacaggccatctgagacacatgcagactatctttgagaactgggcaggttgtagatata
      -----+-----+-----+-----+-----+-----+ 480
a      D  R  P  S  E  T  H  A  D  Y  L  L  R  T  G  Q  V  V  D  I  -
      481  tcagacacatatatacccgaggaaacctgcatgtattgtgaagaagctagattaaagtcc
      -----+-----+-----+-----+-----+-----+ 540
a      S  D  T  I  Y  P  R  N  P  A  M  Y  C  E  E  A  R  L  K  S  -
      541  ttccagaactggccagactatgtctcacctaaccaccaagagagttagcaagtgctggactc
      -----+-----+-----+-----+-----+-----+ 600
a      F  Q  N  W  P  D  Y  A  H  L  T  P  R  E  L  A  S  A  G  L  -
      601  tactacacaggtattgtgaccaagtgcagtgcttttgtgtgtggaactgaaaaat
      -----+-----+-----+-----+-----+-----+ 660
a      Y  Y  T  G  I  G  D  Q  V  Q  C  F  C  C  G  G  K  L  K  N  -
      661  tgggaacctgtgatcgtgcctgtgcagaacacagcgacacttccctaattgcttctt
      -----+-----+-----+-----+-----+-----+ 720
a      W  E  P  C  D  R  A  W  S  E  H  R  R  H  F  P  N  C  F  F  -

```

Fig. 1 (page 2 of 7)

HUMAN xiap

```

721 gtttggccggaatctaataattcgaagtgaatctgatgctgtgagttctgataagaaat
-----+-----+-----+-----+-----+-----+ 780
a   V L G R N L N I R S E S D A V S S D R N -
781 ttcccaattcaacaatctccaagaatccatccatgycagattatgaagcagcagtc
-----+-----+-----+-----+-----+-----+ 840
a   F P N S T N L P R N P S M A D Y E A R I -
841 ttacttttgggacatgatatatactcagttaacaaggagcagcttgcaagagctgattt
-----+-----+-----+-----+-----+-----+ 900
a   F T F G T W I Y S V N K E Q L A R A G F -
901 tatgctttagtgtaagtgataaagtaagtcttccactgtggaggaggctaactgat
-----+-----+-----+-----+-----+-----+ 960
a   Y A L G E G D K V K C F H C G G G L T D -
961 tggaaagccagtgaaagacccttgggaacacatgtctaattgtatccagggtgcaaatat
-----+-----+-----+-----+-----+-----+ 1020
a   W K P S E D P W E Q H A K W Y P G C K Y -
1021 ctgttagaacagaaggacaagaatatataacaatatcatttaactcattcacttgag
-----+-----+-----+-----+-----+-----+ 1080
a   L L E Q K G Q E Y I N N I H L T H S L E -

```

Fig. 1 (page 3 of 7)

HUMAN xip

```

1081 gagtgcgtgtaagaactactgagaacaccacatcactaactagaagaattgatgatacc 1140
-----+-----+-----+-----+-----+-----+
a      E C L V R T T E K T P S L T R R I D D T -
1141 atcttccaaaatccatatgttacaagaagctatacgaatggygttcagttcaaggacatt 1200
-----+-----+-----+-----+-----+-----+
a      I F Q N P M V Q E A I R M G F S F K D I -
1201 aagaaaataatgtgaggaaaaaattcagatatctgygagcaactataaatcacttgaggtt 1260
-----+-----+-----+-----+-----+-----+
a      K K I M E E K I Q I S G S N Y K S L E V -
1261 ctggttcagatctagtgaatgctcagaagaagacagtatgcaagatgagtcagtcagact 1320
-----+-----+-----+-----+-----+-----+
a      L V A D L V N A Q K D S M Q D E S S Q T -
1321 tcattacagaaagagattagttactgaagagcagcctaagcgcctgcaagaggagaagcctt 1380
-----+-----+-----+-----+-----+-----+
a      S L Q K E I S T E E Q L R R L Q E E K L -
1381 tgcaaaatctgtatgtagagaatatgtctatcgttttgttccttgygacatctagtc 1440
-----+-----+-----+-----+-----+-----+

```

Fig. 1 (page 4 of 7)

HUMAN xiap

```

a      C K I C M D R N I A I V F V P C G H L V -
1441  acttgytaacaatgtgtcgaagcagttgacaagtgcccatgtgtcacacagtcattact
-----+-----+-----+-----+-----+-----+
a      T C K Q C A E A V D K C P M C Y T V I T -
1501  ttcaagcaaaaaattttatgtcttaactctaactctatagtaggcattgttattgttct
-----+-----+-----+-----+-----+-----+
a      F K Q K I F M S * -
1561  tattaccctgattgaatgtgtgatgtgaactgactttaagtaatcaggattgaattccat
-----+-----+-----+-----+-----+-----+
a      tagcatttgctaccagaagtaggaaaaaaatgtacatgagcagtgtttagttggcaatata
1621  -----+-----+-----+-----+-----+-----+
a      atcttgaatttcttgatttttcagggtattagctgtatatccattttttactgtta
1681  -----+-----+-----+-----+-----+-----+
a      tttaattgaaaccatagactaagaataagaagcatcatataactgaacacaatggtgt
1741  -----+-----+-----+-----+-----+-----+

```

Fig. 1 (page 5 of 7)

HUMAN xiap

1801 atcctagtcactgatttaatttctaagtgtagtgaaattaatcatctggatttttat
-----+-----+-----+-----+-----+-----+
1860

a

1861 tcttttcagataggcttaacaaatggagcttctgtatatataatgtggagattagagtta
-----+-----+-----+-----+-----+-----+
1920

a

1921 atctccccaatcacataattgttttgtgtgaaaaaggaataaattgttccatgctgtg
-----+-----+-----+-----+-----+-----+
1980

a

1981 gaaagatagagattgtttttagaggttggtgtgtgttttaggattctgtccatttct
-----+-----+-----+-----+-----+-----+
2040

a

2041 tgtaaagmnataaacacgnaentgtgcgaatatnttgttaagtgatttgccattnttg
-----+-----+-----+-----+-----+-----+
2100

a

2101 aaagcgtatttaatgtagaatactatcgagccaacatgtactgacatggaaagatgtca
-----+-----+-----+-----+-----+-----+
2160

a

Fig. 1 (page 6 of 7)

HUMAN xiaop

nagatatgttaagtgtaaaatgcgaagtggcmmacactatgttatagtcctgagccagatca
-----+-----+-----+-----+-----+-----+ 2220

2161

൧

2221 aagtatgtatctttaaataatgcataagaacnaagatttgyaaagatatacaccaactg 2280

३

ttaatgtgcttcctcgcggagggaattggggagggcccgaggggttta
-----+-----+-----+-----+-----+
2281 2340

၃

2341 -----+-----+-----+-----+
 nagggcctttcacttcnactttttcattgttctgttcgnatttttataagtat

മു

gtanaccnagggtttatgmaactaacatcagtaacctaaccccgtagtatact
-----+-----+-----+-----+-----+-----+

၃၃

gtnccttcctagggagctgtntgtttccaccaccaccctccctctgaacaatgc
-----+-----+-----+-----+-----+-----+ 2520
2461

മ

2521 ctgagtgcctgggcaacttn 2540
 -----+-----+

५

Fig. 1 (page 7 of 7)

HUMAN hiap-1

SEQ ID NO:5

1 TCCTTGAGATGTATCAGTATAGGATTAGATCTCCATGTTGGAAGCTAAATGCATAGA
-----+-----+-----+-----+-----+ 60

C

61 AATGGAATAATGGAATTTTCATTTGGCTTTTCAGCCTAGTATTAAGAACTGATAAAA
-----+-----+-----+-----+-----+ 120

C

121 GCAAAGCCATGCACAACACTACCTCCCTAGAGAAGGCTAGTCCCTTTCTCCCATTC
-----+-----+-----+-----+-----+ 180

C

181 ATTCATTATGAACATAGTAAACACGATATCTTATCAATTGATGAAGAAGGCCA
-----+-----+-----+-----+-----+ 240

SEQ ID NO:6

C

241 M N I V E N S I F L S N L M K S A N -
ACACGTTGAACCTGAATAACGACTTGTCACTGTAAGTACCGAATGCTACGTATTCCA
-----+-----+-----+-----+-----+ 300

C

301 T F E L K Y D L S C E L Y R M S T Y S T -
CTTTCCTGCTGGGTTCTCTCTCAGAAGGAGTCTGCTGCTGCTGTTCTAATACA
-----+-----+-----+-----+-----+ 360

C

F P A G V P V S E R S L A R A G F Y Y T -

Fig. 2 (page 1 of 8)

HUMAN hiap-1

```

361 CTGGTGAATGACAAGGTCAATGCTTCTGTGTGGCCCTGATGCTGATACTGAAAA
-----+-----+-----+-----+-----+-----+ 420
      G V N D K V K C F C C G L M L D N W K R -
421 GAGGAGACAGTCCCTACTGAAAGCATAAAAGTTGTATCCTAGCTGCAGATTGCTCAGA
-----+-----+-----+-----+-----+-----+ 480
      G D S P T E K H K K L Y P S C R F V Q S -
481 GTCTAAATCCGTTAACAACCTTGAAGCTACCTCTCAGCCTACTTTCTCTTCACTAA
-----+-----+-----+-----+-----+-----+ 540
      L N S V N N L E A T S Q P T F P S S V T -
541 CACATTCACACACTCATTACTCCGGGTACAGAAACAGTGATATTTCCGTGCTCTT
-----+-----+-----+-----+-----+-----+ 600
      H S T H S L L P G T E N S G Y F R G S Y -
601 ATCAAACTCTCCATCAAAATCCTGTAACCTCCAGAGCAAATCAAGATTCTGCCTGA
-----+-----+-----+-----+-----+-----+ 660
      S N S P S N P V N S R A N Q E F S A L M -
661 TGAGAAGTTCCTACCCCTGTCCAATGAATAACGAAATGCCAGATTACTTTTCAGA
-----+-----+-----+-----+-----+-----+ 720
      R S S Y P C P M N N E N A R L L T F Q T -

```

Fig. 2 (page 2 of 8)

HUMAN hiap-1

```

721 -----+-----+-----+-----+-----+-----+ 780
CATGCCATTGACTTTCTGTCGCCAACAATCTGGCAGCAGCGCTTTACTACATAG

c      W P L T F L S P T D L A R A G F Y Y I G -
781 -----+-----+-----+-----+-----+-----+ 840
GACCTGAGACAGAGTGGCTTGCTTGCTGTGGTGAATAATGAGCAATTGGAAACCGA

c      P G D R V A C F A C G G K L S N W E P K -
841 -----+-----+-----+-----+-----+-----+ 900
AGGATAATGCTATGTCAGAACACCTGAGACATTTCCCAATGCCCATTTATAGAAATC

c      D N A M S E H L R H F P K C P F I E N Q -
901 -----+-----+-----+-----+-----+-----+ 960
AGCTTCAAGACACTTCAAGATACACAGTTCTAATCTGAGCATGACAGACATGCAGCCC

c      L Q D T S R Y T V S N L S M Q T H A A R -
961 -----+-----+-----+-----+-----+-----+ 1020
GCTTAAACATCTTTAACTGGCCCTAGTGTCTAGTTAATCCTGAGCAGCTTGCAA

c      F K T F F N W P S S V L V N P E Q L A S -
1021 -----+-----+-----+-----+-----+-----+ 1080
GTGCGGTTTATATATGTTGGTAACAAGTATGATGTCAAATGCTTTGCTGTATGTTG

c      A G F Y Y V G N S D D V K C F C C D G G -

```

Fig. 2 (page 3 of 8)

HUMAN hiap-1

```

1081 -----+-----+-----+-----+-----+ 1140
      GACTCAGGTGTTGGGAATCTGAGATGATCCATGGGTTCAACATGCCAAGTGGTTCCAA
c    L R C W E S G D D P W V Q H A K W F P R -
1141 -----+-----+-----+-----+-----+ 1200
      GGTGTGAGTACTTGATAAGAATTAAGGACAGGAGTTTCATCCGTCAAGTTCAAGCCAGTT
c    C E Y L I R I K G Q E F I R Q V Q A S Y -
1201 -----+-----+-----+-----+-----+ 1260
      ACCCTCATCTACTGAACAGCTGCTATCCACATCAGACAGCCCGAGAGATGAAATGCAG
c    P H L L E Q L L S T S D S P G D E N A E -
1261 -----+-----+-----+-----+-----+ 1320
      AGTCATCAATTATCCATTGGAACCTGGAGAAGACCATTCAAGAGATGCAATCATGATGA
c    S S I I H L E P G E D H S E D A I M M N -
1321 -----+-----+-----+-----+-----+ 1380
      ATACTCCTGTGATTAATGCTGCCGTGGAATGGGCTTAGTAGAAGCCTGTAACACAGA
c    T P V I N A A V E M G F S R S L V K Q T -
1381 -----+-----+-----+-----+-----+ 1440
      CAGTTCAGAGAAAATCCTAGCAACTGGAGAGAATTATAGACTAGTCAATGATCTTGTGT
c    V Q R K I L A T G E N Y R L V N D L V L -

```

Fig. 2 (page 4 of 8)

HUMAN hiap-1

```

1441 TAGACTTACTCAATGCAGAGATGAATAAGGAGAGAGAGAGAAGCAACTGAGG + 1500
-----+-----+-----+-----+-----+-----+
C D L L N A E D E I R E E R E R A T E E -
1501 AAAAAGATCAATGATTATTAATCCGGAAGATAGAAATGGCACTTTTCAACATT
-----+-----+-----+-----+-----+-----+
C K E S N D L L L I R K N R M A L F Q H L -
1561 TGACTTGTGTAATCCAATCCTGAGTAGTCTACTACTGCCGAATTATTAACAAG
-----+-----+-----+-----+-----+-----+
C T C V I P I L D S L L T A G I I N E Q E -
1621 AACATGATGTTAATAACAGAGACAGACGCTTTACAAGCAAGAACTGATTGATA
-----+-----+-----+-----+-----+-----+
C H D V I K Q K T Q T S L Q A R E L I D T -
1681 CGATTTAGTAAAGGAATATTCAGCCACTGTATTCAGAACTCTCTGCAAGAAGCTG
-----+-----+-----+-----+-----+-----+
C I L V K G N I A A T V F R N S L Q E A E -
1741 AAGCTGTATATGAGCATTTATTGTGCAACAGCAGACATAAATATATCCACAGAAG
-----+-----+-----+-----+-----+-----+
C A V L Y E H L F V Q Q D I K Y I P T E D -

```

Fig. 2 (page 5 of 8)

HUMAN hiap-1

```

1801 ATGTTTCAGATCTACCAGTGGAGAACAATTGGGAGACTACCAGAAGAACAATGTA
-----+-----+-----+-----+-----+-----+ 1860
C      V S D L P V E E Q L R R L P E E R T C K -
1861 AAGTGTATGACAAGAAGTGTCCATAGTGTATTATCCCTGTGGTCATCTAGTAT
-----+-----+-----+-----+-----+ 1920
C      V C M D K E V S I V F I P C G H L V V C -
1921 GCAAAGATTGTGCTCCTTCTTTAAGAAAGTGTCTATTGTAGGAGTACAATCAAGGTA
-----+-----+-----+-----+-----+ 1980
C      K D C A P S L R K C P I C R S T I K G T -
1981 CAGTTCGTACATTCTTTCATGAAGAAGAACCAACATCGTCTAACTTAGAATTAA
-----+-----+-----+-----+-----+ 2040
C      V R T F L S *
2041 TTATTAATGTATTATACTTTAACTTTATCCTAATTGGTTCCCTTAAATTTTATT
-----+-----+-----+-----+-----+ 2100
C      TATTACAACCTCAAAAACATGTTTGTGTACATATTATATATGTATCTAACCATA
2101 -----+-----+-----+-----+-----+ 2160

```

Fig. 2 (page 6 of 8)

HUMAN hip-1

```
2161  TGAACATATATTTTGAAGAACTAAGAGATGATAGGCTTTGTCTTATGAACGAAAAA 2220
      -----+-----+-----+-----+-----+-----+
2221  GAGTAGCACTACAACACAAATATCAATCCAAATTGAGCATTATGAAATGTAAGTG 2280
      -----+-----+-----+-----+-----+-----+
      c
2281  AAGTAAACTTAAGATATTGAGTTAACCTTAAGAATTTAAATATTTGGCATTTGAC 2340
      -----+-----+-----+-----+-----+-----+
      c
2341  TAATACCGGAACATGAAGCCAGGTGTGGTATGTACCTGTAGTCCAGGCTGAGGCA 2400
      -----+-----+-----+-----+-----+-----+
      c
2401  AGAGATTACTTGAGCCCAAGAGTTGAATCCATCCTGGGCAGCATACTGAGACCCTGCC 2460
      -----+-----+-----+-----+-----+-----+
      c
2461  TTTAAAAACXAAACAGKACCAAAKCCAACACGAGGACACATTCTCTGCTTTTGAT 2520
      -----+-----+-----+-----+-----+-----+
      c
```

Fig. 2 (page 7 of 8)

HUMAN hiap-1

2521 CAGTGCCATACATCGAAGGTGTCATATATGTTGAATCACATTTAGGACATGGTGT
-----+-----+-----+-----+-----+-----+ 2580

c
2581 TTTTATAAGAATTCTGTGAGXAAAAATTAAATAAGCAACCKAAATTACTCTTAAAAAA
-----+-----+-----+-----+-----+-----+ 2640

c
2641 AAAAAAAAAAAAAAACTCGAGGGGCCCGTACCAAT
-----+-----+-----+-----+-----+ 2676

c

Fig. 2 (page 8 of 8)

HUMAN hiap-2

SEQ ID NO:7

1 TTAGTTACCTGAAGAAGTTACTACAACCCAAAGAGTTGTGTCTAAGTAGTATCTTGG
-----+-----+-----+-----+-----+ 60

a

61 TAATTCAGAGAGATACTCATCCTTACCTGAATATAACTGAGATAAATCCAGTAAAGAAG
-----+-----+-----+-----+-----+ 120

a

121 TGTAGTAAATTCTACATAAGAGCTATCATTTGATTCTTTTGTGGTGAATCTTAGTT
-----+-----+-----+-----+-----+ 180

a

181 CATGTGAAGAATTTCATGTGAATGTTTAGCTATCAAACAGTACTGTCACTACTCATG
-----+-----+-----+-----+-----+ 240

a

241 CACAAACTGCCCTCCCAAGACTTTCCCAAGTCCCTCGTATCAAAACATTAAGAGTATA
-----+-----+-----+-----+-----+ 300

SEQ ID NO:8 a

H K T A S Q R L F P G P S Y Q N I K S I -
ATGGAAGATAGCAGATCTTGTCAGATTGGACAAACAGCAACAACAAAAATGAAGTAT
-----+-----+-----+-----+-----+ 360

a

M E D S T I L S D W T N S N K Q K M K Y -

Fig. 3 (page 1 of 7)

HUMAN hiap-2

```

a      361      GACTTTCCTGTAAGCTCTACAGAATGCTACATATTCAACTTCCCCGGGGTCCCT
-----+-----+-----+-----+-----+-----+-----+-----+
a      421      D F S C E L Y R M S T Y S T F P A G V P
-----+-----+-----+-----+-----+-----+-----+
a      481      GTCTCAGAAAGAGTCTTGCTCGTCTGTTTATTACTGGTGGAATGACAAGTC
-----+-----+-----+-----+-----+-----+-----+
a      541      V S E R S L A R A G F Y Y T G V N D K V
-----+-----+-----+-----+-----+-----+-----+
a      601      AAATGCTTCTGTGTGGCCTGATGCTGATACTGGAAGACTAGAGACAGTCCTATTCAA
-----+-----+-----+-----+-----+-----+-----+
a      661      K C F C C G L M L D N W K L G D S P I Q
-----+-----+-----+-----+-----+-----+-----+
a      720      AAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTCAGAAATCTGGTTTCAGCTAGTCTG
-----+-----+-----+-----+-----+-----+-----+
a      780      K H K Q L Y P S C S F I Q N L V S A S L
-----+-----+-----+-----+-----+-----+-----+
a      840      GGATCCACCCTTAAGAATACGTCTCCAATGAGAAACAGTTTGACATTCATTATCTCCC
-----+-----+-----+-----+-----+-----+-----+
a      900      G S T S K N T S P M R N S F A H S L S P
-----+-----+-----+-----+-----+-----+-----+
a      961      ACCTTGAACATAGTAGCTTGTTCAGTGGTCTTACTCCAGCCTTCCTCAAACCTCTT
-----+-----+-----+-----+-----+-----+-----+
a      1020      T L E H S S L F S G S Y S S L P P N P L
-----+-----+-----+-----+-----+-----+-----+

```

Fig. 3 (page 2 of 7)

HUMAN hiap-2

```

721  AATTCTAGACGAGTGAAGACATCTCTCATCGAGGACTAACCCCTACAGTTATGCAATG
-----+-----+-----+-----+-----+-----+-----+
a    N S R A V E D I S S S R T N P Y S Y A M -
781  AGTACTGAAGAAGCCAGATTCTTACCTACCATATGTGCCATTACTTTTGTACCA
-----+-----+-----+-----+-----+-----+-----+
a    S T E E A R F L T Y H M W P L T F L S P -
781  TCAGAATTGGCAAGAGCTGTTTATTATATAGGACCTGAGATAGGTTAGCCTGTT
-----+-----+-----+-----+-----+-----+-----+
a    S E L A R A G F Y Y I G P G D R V A C F -
841  GCCTGTGTGGGAAGCTCAGTACTGGAACCAAGGATGCTATGTCAGACACCGG
-----+-----+-----+-----+-----+-----+-----+
a    A C G G K L S N W E P K D D A M S E H R -
901  AGGCATTTCCCACTGTCATTTTGGAAATCTCTAGAACTCTGAGGTTAGCATT
-----+-----+-----+-----+-----+-----+-----+
a    R H F P N C P F L E N S L E T L R F S I -
961  TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTATGTACTGCCATCT
-----+-----+-----+-----+-----+-----+-----+
a    S N L S M Q T H A A R M R T F M Y W P S -
1021

```

Fig. 3 (page 3 of 7)

HUMAN hiap-2

```

a      1081 AGTGTTCAGTTCAGCCTGAGCAGCTTGCAAGTCTGTTTATATATGTTGGTCCGAAT
      -----+-----+-----+-----+-----+ 1140
a      1141 S V P V Q P E Q L A S A G F Y Y V G R N -
      GATGATGTCAAATGCTTTGGTTGTGATGGTGGCTTGAGGTGTGGGAATCTGAGATGAT
      -----+-----+-----+-----+-----+ 1200
a      1201 D D V K C F G C D G G L R C W E S G D D -
      CCATGGGTAGAACATGCCCAAGTGGTTCCAAGGTGTGAGTCTTGATACGAATGAAGGC
      -----+-----+-----+-----+-----+ 1260
a      1261 P W V E H A K W F P R C E F L I R M K G -
      CAAGAGTTGTGATGAGATTCGAAGTAGATAATCCTCATCTTCTGAACAGCTGTGTCA
      -----+-----+-----+-----+-----+ 1320
a      1321 Q E F V D E I Q G R Y P H L L E Q L L S -
      ACTTCAGATACCACTGGAGAAGAAATGCTGACCCACCAATTATTCATTTGGACCTGGA
      -----+-----+-----+-----+-----+ 1380
a      1381 T S D T T G E E N A D P P I I H F G P G -
      GAAAGTCTTCAGAAGATGCTGTATGATGAATACACCTGTGTTAATCTGCCCTTGAA
      -----+-----+-----+-----+-----+ 1440
a      E S S S E D A V M M N T P V V K S A L E -

```

Fig. 3 (page 4 of 7)

HUMAN hiap-2

1441	ATGGCTTTAATAGAGACCTGCTGAACAACAGTTCTAAGTAAATCCTGACAACCTGGA	1500
a	M G F N R D L V K Q T V L S K I L T T G	-
1501	GAGAACTATAAACAAGTAAATGATATGTCAGCACTTCTTAATGCTGAAGATGAAGAAA	1560
a	E N Y K T V N D I V S A L L N A E D E K	-
1561	AGAGAAGAGGAGAAGGAAAAACAAGCTGAAGAATGGCATCAGATGATTGTCATTAAAT	1620
a	R E E E K E K Q A E E M A S	D D L S L I -
1621	CGGAAGACAGAAATGGCTCTTTCAACAATGACATGTGCTTCCTATCCTGGATAAT	1680
a	R K N R M A L F Q Q L T C V L P I L D N	-
1681	CTTTAAAGGCCAATGTAATTATAAACAAGAACATGATATTATTAAACAAAAACACAG	1740
a	L L K A N V I N K Q E H D I I K Q K T Q	-
1741	ATACCTTTACAAGCGAGAGAACTGATTGATACCATTTGGGTTAAGGAATGCTGGGCC	1800
a	I P L Q A R E L I D T I W V K	G N A A A -

Fig. 3 (page 5 of 7)

HUMAN hiap-2

```
1801 AACATCTCAAAACTGTCTAAAGAATGACTCTACATTGTATAAGAACTATTGTG
-----+-----+-----+-----+-----+-----+
a   N I F K N C L K E I D S T L Y K N L F V -
1861 GATAAGAATATGAAGTATATTCACACAGAAGATGTTTCAGGTCTGTCACTGAAGACAA
-----+-----+-----+-----+-----+-----+
a   D K N M K Y I P T E D V S G L S L E E Q -
1921 TTGAGGAGGTTCAGAAGAAGACGAAGTGTAAAGTGTATGGACCAAGAAGTTCTGTT
-----+-----+-----+-----+-----+-----+
a   L R R L Q E E R T C K V C M D K E V S V -
1981 GTATTATTCCCTTGTGTCATCTGCTAGTATGCCAGGAATGCCCCCTTCTCTAAGAAA
-----+-----+-----+-----+-----+-----+
a   V F I P C G H L V V C Q E C A P S L R K -
2041 TGCCCTATTGCAAGGGTATAATCAAGGTAAGTCTGTTGACATTCTCTTAAGAAAA
-----+-----+-----+-----+-----+-----+
a   C P I C R G I I K G T V R T F L S * -
2101 ATAGTCTATATTTAACCTGCATAAAAGGCTTTAAATATGTTGAACACTTGAAGCC
-----+-----+-----+-----+-----+-----+
a   2160
```

Fig. 3 (page 6 of 7)

HUMAN hiap-2

2161 ATCTAAAGTAAAAGGAATTAGAGTTTTC AATTAGTAACATT CATGTTCTAGTCTGC
-----+-----+-----+-----+-----+-----+
a
2221 TTGGTACTAATAATCTGTTTCTGAAAAGATGGTATCATATATTTAATCTTAATCTGTT
-----+-----+-----+-----+-----+-----+
a
2281 TATTACAAGGGAAGATTATGTTTGGTGAAC TATATTAGTATGTATGTACCTAAGGG
-----+-----+-----+-----+-----+-----+
a
2341 AGTAGCGTCXCTGCTGTGTTATGCATCATTTCA GAGTTACTGGATTGTGTTCTTTCAAG
-----+-----+-----+-----+-----+-----+
a
2401 AAAGCTTGAAXACTAAATTATAGTGTAGAAAAGAACTGGAACCAAGAACTCTGGAGTT
-----+-----+-----+-----+-----+-----+
a
2461 CATCAGAGTTATGGTGCCGAATTGCTTTGGTGCTTTTCACTGTGTTTAAATAAGGA
-----+-----+-----+-----+-----+-----+
a
2521 TTTTCTCTAATTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTGCTTTAAAG
-----+-----+-----+-----+-----+-----+
a
2580

Fig. 3 (page 7 of 7)

MOUSE xiap

SEQ ID NO:9

1 GACACTCTGCTGGGGGGGGGGCCCTCCTCCGGACCTCCCCCTGGGAACGTCGCC
-----+-----+-----+-----+-----+-----+ 60

a

61 GCGGCGCTTAGTGAAGCTGAGTCTTGCGCGGAAGGTGACAAGTCCATTTC
-----+-----+-----+-----+-----+-----+ 120

a

121 GAGAAGATGACTTTAACAGTTTGAAGAACTAGAATTGTACTTGACAGACCAAT
-----+-----+-----+-----+-----+-----+ 180

SEQ ID NO:10 a

M T F N S F E G T R T F V L A D T N -
181 AAGATGAAGAATTGTAGAAGAGTTAATAGATTAAAAACATTGTACTTCCCAAGT
-----+-----+-----+-----+-----+-----+ 240

a

K D E E F V E E F N R L K T F A N F P S -
241 AGTAGTCTGTTTCAGCATCAACATTGGCGGAGCTGGTTCTTATACCGGTGAAGA
-----+-----+-----+-----+-----+-----+ 300

a

S S P V S A S T L A R A G F L Y T G E G -
301 GACACCGTCAATGTTTCAGTTGTATGCGCAATAGATGACGATGAGACTCA
-----+-----+-----+-----+-----+-----+ 360

a

D T V Q C F S C H A A I D R W Q Y G D S -

Fig. 4 (page 1 of 6)

MOUSE xiap

```

361  GCTGTGGAAGACACAGAGAATATCCCAATTGCAGATTATCAATGTTTATT
-----+-----+-----+-----+-----+-----+
a   A V G R H R R I S P N C R F I N G F Y F -
421  GAAAATGGTCTGCACAGTCTACAAATCCTGGTATCCAAAATGGCCAGTACAAATCTGAA
-----+-----+-----+-----+-----+-----+
a   E N G A A Q S T N P G I Q N G Q Y K S E -
481  AACTGTGGGAAATAGAAATCCTTTGGCCCTGACAGGCCACCTGAGACTCATGCTGAT
-----+-----+-----+-----+-----+-----+
a   N C V G N R N P F A P D R P P E T H A D -
541  TATCTCTGAGAACTGGACAGGTTGTAGATATTTCAGACACCATATACCGAGAACCT
-----+-----+-----+-----+-----+-----+
a   Y L L R T G Q V V D I S D T I Y P R N P -
601  GCCATGTGTAGTGAAGAGCCAGATTGAAGTCATTTCAGAACTGGCCGGAATGCTCAT
-----+-----+-----+-----+-----+-----+
a   A M C S E E A R L K S F Q N W P D Y A H -
661  TTAACCCCAAGAGAGTAGTAGTGTGGCTCTACTACACAGGGGCTGATGATCAAGTG
-----+-----+-----+-----+-----+-----+
a   L T P R E L A S A G L Y Y T G A D D Q V -
720

```

Fig. 4 (page 2 of 6)

MOUSE xiap

```

a      721  CAATGCTTTTGTGTGGGGAACGAAATGGGAACCTGTGATCGTGCCTGTCA
      -----+-----+-----+-----+-----+ 780
a      Q C F C C G G K L K N W E P C D R A W S -
      781  GAACACAGGAGACACTTCCCAATTGCTTTTGTGTTGGCCGGAACGTTAATGTTGCA
      -----+-----+-----+-----+-----+ 840
a      E H R R H F P N C F F V L G R N V N V R -
      841  AGTGAATCTGGTGTGAGTCTGATAGGAATTTCCAATTCACAACAACCTCTCAAGAAAT
      -----+-----+-----+-----+-----+ 900
a      S E S G V S S D R N F P N S T N S P R N -
      901  CCAGCCATGGCAGAATATGAAGCAGCATCTACTTTTGAACATGGATATACTCAGTT
      -----+-----+-----+-----+-----+ 960
a      P A M A E Y E A R I V T F G T W I Y S V -
      961  AACACGAGCAGCTTGCAAGAGCTGATTATTAGCTTGAAGCGGATAAGTGAAG
      -----+-----+-----+-----+-----+ 1020
a      N K E Q L A R A G F Y A L G E G D K V K -
      1021  TGCCTTCCACTGTGAGGAGGCTCAGGATTTGAAGCCAAGTGAAGACCCCTGGACACAG
      -----+-----+-----+-----+-----+ 1080
a      C F H C G G G L T D W K P S E D P W D Q -

```

Fig. 4 (page 3 of 6)

MOUSE xiap

```

1081 CATGCTAAGTGTACCAGGCTGCAAAATACCTATTGGATGAGAAGGGCAAGATATATA 1140
-----+-----+-----+-----+-----+-----+-----+
a   H A K C Y P G C K Y L L D E K G Q E Y I -
1141 AATAATATTCATTTAACCCATCCACTTGAGGAATCTTTGGAGAAGACTGCTGAAAAACA
-----+-----+-----+-----+-----+-----+-----+
a   N N I H L T H P L E E S L G R T A E K T -
1201 CCACCGCTAACTAAAAAATCGATGATACCATCTCCAGAATCCTATGGTCAAGAAGCT
-----+-----+-----+-----+-----+-----+-----+
a   P P L T K K I D D T I F Q N P M V Q E A -
1261 ATACGAATGGATTGCTTCAAGGACCTTAAGAAACAATGGAAGAAAAATCCAACA
-----+-----+-----+-----+-----+-----+-----+
a   I R M G F S F K D L K K T M E E K I Q T -
TCCGGAGCAGCTATCTATCACTTGAGGTCCTGATTGCAGATCTGTGAGTGCTCAGAAA
1321 -----+-----+-----+-----+-----+-----+ 1380
a   S G S S Y L S L E V L I A D L V S A Q K -
1381 GATAATACGAGAGTGAGTCAAGTCAAACTTCATTGCAGAAAGACATTAGTACTGAAGAG
-----+-----+-----+-----+-----+-----+-----+
a   D N T E D E S S Q T S L Q K D I S T E E -

```

Fig. 4 (page 4 of 6)

MOUSE xiap

```

1441 CAGCTAAGGCGCCTACAAGAGGAAGCTTCCAAATCTGTATGGATAGAATATTGCT
-----+-----+-----+-----+-----+-----+-----+
a    Q L R R L Q E E K L S K I C M D R N I A -
1501 ATCGTTTTTTTCCCTTGTGGACATCTGGCCACTTGTAACAGTGTGCAGAGCAGTTGAC
-----+-----+-----+-----+-----+-----+-----+
a    I V F F P C G H L A T C K Q C A E A V D -
1561 AAATGCCCATGTGCTACACCGTCATTACGTTCAACCAAAAATTTTATGCTTAGTGG
-----+-----+-----+-----+-----+-----+-----+
a    K C P M C Y T V I T F N Q K I F M S * -
1621 GGCACCATGTATGTCTCTTGTCTTAATGAATGTGTAATGGAGCGAATTAG
-----+-----+-----+-----+-----+-----+-----+
a
1681 TAATCCTGCATTGCATTCCATTAGCATCCTGCTGTTCCAAATGGAGACCAATGCTAAC
-----+-----+-----+-----+-----+-----+-----+
a
1741 AGCACTGTTCCGCTTAACATTCATTTCGGATCTTCGAGTTATCAGCTGTATCATT
-----+-----+-----+-----+-----+-----+-----+
a

```

Fig. 4 (page 5 of 6)

MOUSE xiap

a
1801 TAGCCAGTGTTTTACTCGATTGAACCTTAGACAGAGAAGCATTTTATAGCTTTTCACAT
-----+-----+-----+-----+-----+-----+-----+
1860

a
1861 GTATATTGGTAGTACACTGACTTGATTCTATATGTAAGTGAATTCACCTGCATGTT
-----+-----+-----+-----+-----+-----+-----+
1920

a
1921 TCATGCCCTTTTGCATAAGCTTAACAAATGAGTGTCTGTATAAGCATGGAGATGTGATG
-----+-----+-----+-----+-----+-----+-----+
1980

a
1981 GAATCTGCCCAATGACTTTAATTGGCTTATTGTAACACGAAAGAACTGCCCCACGCTG
-----+-----+-----+-----+-----+-----+-----+
2040

a
2041 CTGGAGGATAAGATTGTTTAGATGCTCACTTCTGTGTTTAGGATTCTGCCCATTTA
-----+-----+-----+-----+-----+-----+-----+
2100

Fig. 4 (page 6 of 6)

M-hiap-1

SEQ ID NO:39

```

GAATTCGGGAGACCTACACCCCGAGATCAGAGTCATTGCTGGCCTTCAAGCCTAG
1  -----+-----+-----+-----+-----+ 60
GAAGTGGGCTGCGGTATCAGCCTAGCAGTAAACCGACGAGGACCATGCACAAACTAC
61  -----+-----+-----+-----+-----+ 120
ATCCCCAGAGAAAGACTGTCCCTTCCCTCCCTGTCATCTCACCATGAACATGTTCAA
121 -----+-----+-----+-----+-----+ 180
M N M V Q -

```

SEQ ID NO:40

```

GACAGCGCCTTTCTAGCCAAAGCTGATGAAGAGTGTGACACCTTTGAGTTGAAGTATGAC
181 -----+-----+-----+-----+-----+ 240
D S A F L A K L M K S A D T F E L K Y D -
TTTTCCTGTAGCTGTACCGATTGTCCACGTATTCAGCTTTCCCAAGGAGTTCCTGTG
241 -----+-----+-----+-----+-----+ 300
F S C E L Y R L S T Y S A F D R G V P V -
TCAGAAAGGAGTCTGGCTCGTGTGCTTTTACTACTGCTGGTCCAATGACAAGGTCAAG
301 -----+-----+-----+-----+-----+ 360
S E R S L A R A G F Y Y T G A N D K V K -
TGCTTCTGCTGTGGCCTGATGCTAGACAAGTGAACAAGGGACAGTCCCATGGAGAAG
361 -----+-----+-----+-----+-----+ 420
C F C C G L M L D N W K Q G D S P M E K -

```

Fig. 5 (page 1 of 6)

M-hiap-1

```

421 -----+-----+-----+-----+-----+ 480
    CACAGAAAGTTGTACCCCAAGCTGCACTTGTACAGACTTTGAATCCAGCCAACAGTCTG
    H R K L Y P S C N F V Q T L N P A N S L
    -----+-----+-----+-----+-----+

481 -----+-----+-----+-----+-----+ 540
    GAAGCTAGTCCTCGGCCCTTCTTCTTCCACGGCGATGAGCACCATTGCCCTTGAGCTTT
    E A S P R P S L P S T A M S T M P L S F
    -----+-----+-----+-----+-----+

541 -----+-----+-----+-----+-----+ 600
    GCAAGTTCTGAGAATACTGGCTATTTCAGTGGCTCTTACTCGAGCTTCCCTCAGACCCT
    A S S E N T G Y F S G S Y S S F P S D P
    -----+-----+-----+-----+-----+

601 -----+-----+-----+-----+-----+ 660
    GTGAAGTTCCGAGCAATCAAGATTGTCTGCTTGGAGCACAAGTCCCTACCACTTTGCA
    V N F R A N Q D C P A L S T S P Y H F A
    -----+-----+-----+-----+-----+

661 -----+-----+-----+-----+-----+ 720
    ATGAACACAGAGAAGGCCAGATTACTCACTATGAACATGCCATTGTCTTCTGTCA
    M N T E K A R L L T Y E T W P L S F L S
    -----+-----+-----+-----+-----+

721 -----+-----+-----+-----+-----+ 780
    CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGGACCTGGAGATAGAGTGGCCTGC
    P A K L A K A G F Y Y I G P G D R V A C
    -----+-----+-----+-----+-----+

```

Fig. 5 (page 2 of 6)

M-hiap-1

```

781  TTTGCGTGCATGGAACTGAGCACTGGAACTGGAAGTATGATGCTATGTCAGAGCAC
-----+-----+-----+-----+-----+-----+-----+-----+
F A C D G K L S N W E R K D D A M S E H - 840
841  CAGAGGCATTCCCCAGCTGTCGGTCTTALLKACTTGGGTCACTGCTTCGAGATAC
-----+-----+-----+-----+-----+-----+-----+-----+
Q R H F P S C P F L K D L G Q S A S R Y - 900
901  ACTGTCTTAACCTGAGCATGACACACGACGCCGTATTAGACATCTCTAACTGG
-----+-----+-----+-----+-----+-----+-----+-----+
T V S N L S M Q T H A A R I R T F S N W - 960
961  CCTTCTAGTGCACTAGTTCATTCGCCAGAACTGCAAGTGGGGCTTTATTATACAGGA
-----+-----+-----+-----+-----+-----+-----+-----+
P S S A L V H S Q E L A S A G F Y Y T G - 1020
1021  CACAGTGATGATGCAAGTGTATTATGCTGTGATGGTGGCTGAGGTGCTGGGAATCTGGA
-----+-----+-----+-----+-----+-----+-----+-----+
H S D D V K C L C C D G G L R C W E S G - 1080
1081  GATGACCCCTGGGTGAACATGCCAAGTGGTTCCAAGGTGTGAGTACTTGTCTCAGAATC
-----+-----+-----+-----+-----+-----+-----+-----+
D D P W V E H A K W F P R C E Y L L R I - 1140
1141  AAAGCCAAGAATTGTGACCCAAGTTCAGCTGGCTATCCTCATCTACTTGAGCAGCTA
-----+-----+-----+-----+-----+-----+-----+-----+
K G Q E F V S Q V Q A G Y P H L L E Q L - 1200

```

Fig. 5 (page 3 of 6)

M-hiap-1

```

1201 TTATCTACGTCAGACTCCCCAGAAGATGAAATGCAGACGCAGCAATCGTCATTGGC
-----+-----+-----+-----+-----+-----+-----+
L S T S D S P E D E N A D A A I V H F G - 1260
CCTGGAGAAAGTTCGGAAGATGTCGTCATGATGAGCAGCGCTGTGTTAAGCAGCCTTG
1261 -----+-----+-----+-----+-----+-----+-----+
P G E S S E D V V M M S T P V V K A A L - 1320
GAAATGGGCTTCACTAGGAGCCCTGGTGAGACAGACGGTTCACTGGCAGATCCTGCCACT
1321 -----+-----+-----+-----+-----+-----+-----+
E M G E S R S L V R Q T V Q W Q I L A T - 1380
GGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATGCAGAAGACGAG
1381 -----+-----+-----+-----+-----+-----+-----+
G E N Y R T V S D L V I G L L D A E D E - 1440
ATGAGAGAGAGCAGATGAGCAGCGCGCCGAGGAGGAGGAGTCAGATGATCTAGCACTA
1441 -----+-----+-----+-----+-----+-----+-----+
M R E E Q M E Q A A E E E E S D D L A L - 1500
ATCCGGAAGAACAAATGTGCTTTTCCAACATTGACGTGTGTGACACCAATGCTGTAT
1501 -----+-----+-----+-----+-----+-----+-----+
I R K N K M V L F Q H L T C V T P M L Y - 1560

```

Fig. 5 (page 4 of 6)

M-hiap-1

```

1561 TGCCTCCTAAGTGAAGGCCATCACTGAACAGAGTGCATGCTGTGAACAGAAACCA
-----+-----+-----+-----+-----+-----+
C L L S A R A I T E Q E C N A V K Q K P - 1620
1621 CACACCTTACAAGCAAGCACACTGATTGATACTGTGTAGCAAAGGAACACTGCAGCA
-----+-----+-----+-----+-----+-----+
H T L Q A S T L I D T V L A K G N T A A - 1680
1681 ACCTCATTCAGAACTCCCTTCGGGAATTGACCCCTGCTATACAGAGATATTTGTG
-----+-----+-----+-----+-----+-----+
T S F R N S L R E I D P A L Y R D I F V - 1740
1741 CAACAGGACATTAGGAGTCTTCCACAGATGACATTGCAGCTCTACCAATGGAAGACAG
-----+-----+-----+-----+-----+-----+
Q Q D I R S L P T D D I A A L P M E E Q - 1800
1801 TTGCGGCCCTCCCGAGAGACAGATGTAAAGTGTATGACCGAGAGGTATCCATC
-----+-----+-----+-----+-----+-----+
L R P L P E D R M C K V C M D R E V S I - 1860
1861 GTGTTCAATCCCTGTGGCATCTGTCGTGCAAAAGACTGCGCTCCCTCTTGAGGAAG
-----+-----+-----+-----+-----+-----+
V F I P C G H L V V C K D C A P S L R K - 1920

```

Fig. 5 (page 5 of 6)

M-hiap-1

```

1921  TGTCCCATCTGTAGAGGACCATCAAGGACAGTGGCACATTCTCTGAAACAAGA
      -----+-----+-----+-----+-----+-----+
      C P I C R G T I K G T V R T F L S *
1980  -----+-----+-----+-----+-----+-----+

1981  CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACCTGTCACTCCCA GTTCCAT
      -----+-----+-----+-----+-----+-----+
2040  TCGGAAC TTGAGGCCAGCCTGGATAGCAGACACCGCCAACKCAAAATATAA ACAT
      -----+-----+-----+-----+-----+-----+
2041  GAAAAA CTTTGTCTGAAGTCAAGAATGAATTA CTATATAATAATTTAATTGGT
      -----+-----+-----+-----+-----+-----+
2101  TTCCTTAAAGTGCTATTGTTCCCAACTCAGAAATGTTTCTGTAAACATATTACA
      -----+-----+-----+-----+-----+-----+
2161  TACTACCTGCATCTAAAGTATTCATATATTCA TATATTCAGATGTCATGAGAGGGTTT
      -----+-----+-----+-----+-----+-----+
2221  TGTTC TTGTTCTTGAAAAGCTGGTTATCATCTGATCAGCATATACTGCCAACGGCAG
      -----+-----+-----+-----+-----+-----+
2281  GGCTAGAATCCATGAACCAAGCTGCAAAGATCTC ACGCTAAATAAGCGGAAAGATTGG
      -----+-----+-----+-----+-----+-----+
2341  AGAAACGAAAGGAAATTCTTCTCTGTCCAATG TACTCTTCAGACTAATGACCTCTTCC
      -----+-----+-----+-----+-----+-----+
2401  TATCAAGCCTTCTA
2461  -----+-----+-----+-----+-----+-----+
      2474

```

Fig. 5 (page 6 of 6)

M-hiap-2

SEQ ID NO:41

CTGTGGTGAGATCTATGTGCCAAGTGGTGAGAACTTCATCTGGAAGTTAAGCGGTCA
 1 -----+-----+-----+-----+-----+-----+ 60
 GAAATACTATTACTACTCATGACAKRACGTCTCCAGAGACTCGCCCAAGTACCTTA
 61 -----+-----+-----+-----+-----+-----+ 120
 CACCCRAAACTTAACGTATAATGAGAAGAGCACAATCTTGTCAAATTGACAAAGGA
 121 -----+-----+-----+-----+-----+-----+ 180

SEQ ID NO:42

M E K S T I L S N W T K E -
 GAGCGAAGAAAAATGAAGTTGACTTTTCGTGGAAGTCTACCGAATGCTACATATTC
 181 -----+-----+-----+-----+-----+-----+ 240
 S E E K M K F D F S C E L Y R M S T Y S -
 AGCTTTCCCAAGGGAGTCCCTGTCTCAGAGAAGAGTCTGGCTCGTGGCTTTTATTA
 241 -----+-----+-----+-----+-----+-----+ 300
 A F P R G V P V S E R S L A R A G F Y Y -
 TACAGGTGTAATGACAAGTCAAGTGTCTTCTGTGTGGCCTGATGTGATACTGAA
 301 -----+-----+-----+-----+-----+-----+ 360
 T G V N D K V K C F C C G L M L D N W K -
 ACAAGGGGACAGTCTGTGAAAAGCACAGACAGTCTATCCAGCTGCAGCTTTGTACA
 361 -----+-----+-----+-----+-----+-----+ 420
 Q G D S P V E K H R Q F Y P S C S F V Q -

Fig. 6 (page 1 of 6)

M-hiip-2

```

421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GACTCTGCTTCAGCCAGTCTGCAGTCTCCATCTAGAATATGTCCTGTAAGTAG
T L L S A S L Q S P S K N M S P V K S R -
480

ATTGCACATTCGTACCTCTGGAACGAGGTGCATTCCTCCAACCTGTGCTAGCCC
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
F A H S S P L E R G G I H S N L C S S P -
540

TCTTAATCTAGACAGTGAAGACTTCTCATCAAGATGATCCCTGCAGCTATGCCAT
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
L N S R A V E D F S S R M D P C S Y A M -
600

GAGTACAGAAGGCCAGATTCTTACTTACAGTATGCGCCTTAAATTCTGTCAAC
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
S T E E A R F L T Y S M W P L S F L S P -
660

AGCAGAGCTGGCCAGAGCTGGCTTATTACATAGGCCCTGGAGACAGGGTGGCCTGTT
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
A E L A R A G F Y Y I G P G D R V A C F -
720

TGCCCTGTGGTGGAACTGAGCAACTGGGAACCAAGATTATGCTATGTCAGAGCACCG
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
A C G G K L S N W E P K D Y A M S E H R -
780

```

Fig. 6 (page 2 of 6)

M-hiap-2

```

781 -----+-----+-----+-----+-----+-----+-----+ 840
CAGACATTTCCCCACTGTCATTCTTGAAATACTTCAGAAACACAGAGTTTAGTAT
R H F P H C P F L E N T S E T Q R F S I -
ATCAAATCTAGTATGCAGACACACTCTGCTGATTGAGGACATTCTGTACTGCCACC
841 -----+-----+-----+-----+-----+-----+-----+ 900
S N L S M Q T H S A R L R T F L Y W P P -
TAGTCTTCTGTTCAGCCCGAGCAGCTTGCAAGTCTGATTCATTAACGTGATCGCRA
901 -----+-----+-----+-----+-----+-----+-----+ 960
S V P V Q P E Q L A S A G F Y Y V D R N -
TGATGATGTCAGTCCCTTGTGTGATGGTGGCTTGAGATGTTGGAACTGGAGATGA
961 -----+-----+-----+-----+-----+-----+-----+ 1020
D D V K C L C C D G G L R C W E P G D D -
CCCCTGATAGAACACGCCAATGTTCCAAAGGTGAGTCTTGATACGGATGAAGG
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
P W I E H A K W F P R C E F L I R M K G -
TCAGGAGTTGTGATGAGATTCAAGCTAGATATCCTCATCTTCTTGAGCAGCTGTGTC
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
Q E F V D E I Q A R Y P H L L E Q L L S -

```

Fig. 6 (page 3 of 6)

M-hiap-2

```

1141 CACTTCAGACACCCAGGAGAGAATAATGCTGACCCCTACAGACAGTGGTGCATTGG
-----+-----+-----+-----+-----+-----+
T S D T P G E E N A D P T E T V V H F G - 1200

1201 CCCTGGAGAAAGTTGAAAGATGTCGTGATGAGCACGCCCTGTGTTAAAGCAGCCTT
-----+-----+-----+-----+-----+-----+
P G E S S K D V V M M S T P V V K A A L - 1260

1261 GGAATGGGCTTCAGTAGGACCTGTGAGACAGACGGTTCAGCGGAGATCCTGGCCAC
-----+-----+-----+-----+-----+-----+
E M G F S R S L V R Q T V Q R Q I L A T - 1320

1321 TGGTGAGACTACAGACCCGTCATGATATTGCTCTCAGTACTTTGAATGCTGAAGATGA
-----+-----+-----+-----+-----+-----+
G E N Y R T V N D I V S V L L N A E D E - 1380

1381 GAGAAGAGAAGAGAGAAGACAAGACAGACTGAAGAGATGGCATCAGGTGACTTATCACT
-----+-----+-----+-----+-----+-----+
R R E E E K E R Q T E E M A S G D L S L - 1440

1441 GATTCCGAAGATAGAAATGGCCCTCTTCAACAGTTGACACATGTCCTTCCATCCTGGA
-----+-----+-----+-----+-----+-----+
I R K N R M A L E Q Q L T H V L P I L D - 1500

```

Fig. 6 (page 4 of 6)

M-hiap-2

```

1501  TAATCTTCTTGAGGCCAGTGAATTACAAACAGGAACATGATATTATTAGACAGAAAAC
-----+-----+-----+-----+-----+-----+-----+
      N L L E A S V I T K Q E H D I I R Q K T - 1560
1561  ACAGATACCCCTTACAAGCAAGAGAGCTTATTGACACCGTTTGTAGTCAAGGGAATGCTGC
-----+-----+-----+-----+-----+-----+-----+
      Q I P L Q A R E L I D T V L V K G N A A - 1620
1621  AGCCAACATCTTCAAAACTCTCTGAAGGAATTGACTCCACGTTATATGAAACTTATT
-----+-----+-----+-----+-----+-----+-----+
      A N I F K N S L K G I D S T L Y E N L F - 1680
1681  TGTGGAAGAATATGAAGTATATTCCAACAGAGACGTTTCAGGCTTGTCATTGGAAGA
-----+-----+-----+-----+-----+-----+-----+
      V E K N M K Y I P T E D V S G L S L E E - 1740
1741  GCAGTTCGGAGATTACAAGAAGACCACTTGCAAGTGTATGACAGAGAGGTTTC
-----+-----+-----+-----+-----+-----+-----+
      Q L R R L Q E E R T C K V C M D R E V S - 1800
1801  TATTGTGTCATTCCGTTGTCATCTAGTAGTCTGCCAGGAATGCCCCCTCTCTAAG
-----+-----+-----+-----+-----+-----+-----+
      I V F I P C G H L V V C Q E C A P S L R - 1860

```

Fig. 6 (page 5 of 6)

M-hiap-2

```

1861 -----+-----+-----+-----+-----+-----+ 1920
      GAAGTCCCCCATCTGCAGGGGGACAATCAAGGGAGCTGTGGCACAATTCTCATGAGT
      K C P I C R G T I K G T V R T F L S * -
1921 -----+-----+-----+-----+-----+-----+ 1980
      GAAGAATGGTCTGAAGAATTTGTTGACATCAGAAAGCTGTCAGACAAGAATGAACACTAC
      TGATTTCAAGCTCTTCAGCAGGACATTTACTCTCTTCAAGATTAGTAATCTTGCTTTAT
1981 -----+-----+-----+-----+-----+-----+ 2040
      GAAGGTAAGCATTTGATATTAAAGCTTAGTCTGTGCAAGGGAAGGCTATGCTGTTGAG
      -----+-----+-----+-----+-----+-----+ 2100
2041 -----+-----+-----+-----+-----+-----+ 2160
      CTACAGGACTGTGTCTGTTCCAGAGCAGAGTTGGATGCTTGCTGTATGTCCTTCAGGA
2101 -----+-----+-----+-----+-----+-----+ 2160
      CTTCTTGGATTGGGAATTTGGGAAAGCTTTGGAATCCAGTATGTGAGCTCAGAAA
2161 -----+-----+-----+-----+-----+-----+ 2220
      TCCTGGAACCAAGTACTCTGGTACTCAGTAGATAGGGTACCCTGTACTTCTTGGTGCTTT
2221 -----+-----+-----+-----+-----+-----+ 2280
      TCCAGTCTGGGAATAAGGAGGAATCTGCTGCTGTAATAATTGCTGATGTGAGAAAT
2281 -----+-----+-----+-----+-----+-----+ 2340
      AGATGAAAGTGTTCGGGTGGGGCGTGCATCAGTGTAGTGTGTGCAAGGATGTATGCAG
2341 -----+-----+-----+-----+-----+-----+ 2400
      GCCAAACACTGTGTAG
2401 -----+-----+-----+-----+-----+-----+ 2416

```

Fig. 6 (page 6 of 6)

Alignment of BIR (Baculoviral IAP Repeats) Domains

Baculovirus		<i>Cydia pomonella</i>
Cp_iap		<i>Orgyia pseudotsugata</i>
Op_iap		
Human		IAP on X chromosome
xiap		two different human IAP genes
hiap1, hiap2		
Mouse		mouse homologue of human xiap gene
m-xiap		
Insect		<i>Drosophila</i> IAP gene, not clearly a homologue of xiap or hiap
diap		
note on consensus:		The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence.
SEQ ID NO:11	Op_iap-1	1
SEQ ID NO:14	Cp_iap-1	
SEQ ID NO:15	diap-2	
SEQ ID NO:16	m-xiap-1	
SEQ ID NO:17	xiap-1	
SEQ ID NO:18	hiap1-1	
SEQ ID NO:19	hiap2-1	
SEQ ID NO:20	m-xiap-2	
SEQ ID NO:21	xiap-2	
SEQ ID NO:22	hiap1-2	
SEQ ID NO:23	hiap2-2	
SEQ ID NO:24	m-xiap-3	
SEQ ID NO:25	xiap-3	
SEQ ID NO:26	hiap1-3	
SEQ ID NO:27	hiap2-3	
SEQ ID NO:28	Op_iap-2	
SEQ ID NO:29	Cp_iap-2	
SEQ ID NO:30	diap-3	
SEQ ID NO:31	diap-1	
SEQ ID NO:2	Consensus	
		kaarLgTYtn WPvqf.leps rMAasGFYYI GrGDeVrCaf CkveItmWvr gDdpetdHkr waPqCpFV eevRLnTFek WPvst.lspe tMAkNGFYI GrsDeVrCaf CkveImrWke gEdpaadHkK waPqCpFV eanRLvTFkd WPnqn.ilpq aLAKAGFYI nrlDhVkcVw CngvIakWek ndnafeeHkr ffpqCpFV efnRLkTFan FPssspvsas tLArAGFLYt GegDtVqCfs ChaaidrWqy gDsavgrHrr isPncrFI efnRLkTFan FPsgspvsas tLArAGFLYt GegDtVrCfs ChaavdrWqy gDsavgrHrk vsPncrFI elyRMstYst FPagvpvser sLArAGFYt GvndKvKcFc CgImldnWkI gDspiqkHkK lYPscrfV elyRMstYst FPagvpvser sLArAGFYt GvndKvKcFc CgImldnWkI gDspiqkHkK lYPscrfV eearLksFqn WPDyahltpr eLAsAGLYt GaddqVqCfc CgsklknWep cDraWseHrr hfpnCifV eearLksFqn WPDyahltpr eLAsAGLYt GaddqVqCfc CgsklknWep cDraWseHrr hfpnCifV eearLksFqn WPDyahltpr eLAsAGLYt GaddqVqCfc CgsklknWep cDraWseHrr hfpnCifV enaRLlTFqt WP.lIfIspt dLArAGFYI GpgDrVAcFa CgsklknWep kDdamseHrr hfpnCpFI eearLlTFhm WP.lIfIsps eLArAGFYI GpgDrVAcFa CgsklknWep kDdamseHrr hfpnCpFI yearLlTFgt Wiysv..nke qLArAGFYal GegDkVkcFh CgggltdWkp sEdpweqHak wYPgCkYl yearLlTFgt Wiysv..nke qLArAGFYal GegDkVkcFh CgggltdWkp sEdpweqHak wYPgCkYl haARkTFtn WPssvlvnpqe qLAsAGFYV GnsdDvkCfc CdggllrcWes gDdpwvqHak wfpRceFI haARkTFtn WPssvlvnpqe qLAsAGFYV GnsdDvkCfc CdggllrcWes gDdpwvqHak wfpRceFI haARmRTFmy WPssvpvqpe qLAsAGFYV GnsdDvkCfc CdggllrcWes gDdpwvqHak wfpRceFI eaARlRTFaE WPrglkqrpe eLaeAGFYt GggbDktrCfc Cdggllkdwep dDapwqgHar wYdrceYV eaARvksFhn WPrmkqrpe qMAdAGFYt GyDntkCFy Cdggllkdwep edvPweqHrr wIdrcayV vdaRLrTFtd WPisnigpas aLaqAGLYtYq kIgdqVrCFh Cniglrswqk edepwieHak wSPkCqFV esvRLaTFge WPlnapvsae dLvanGF.. GtwmeaeCdf ChvridrWey gDlvaerHrr sSPicSmV ---RL-TF-- WP----- -LA-AGFY- G--D-V-CF- C-----W-- -D-----H-- --P-C-FV

Fig. 7

SEQ ID NO:12	cp-iap	1	50
SEQ ID NO:13	diap	mtelgmlees	l..naPVSaedl
SEQ ID NO:10	m-xiap	..mtfnstfe	gtrtfvlnad
SEQ ID NO:4	xiap	..mtfnstfe	gsktcvpadi
SEQ ID NO:6	hiap1	mnivensifi	snlmksantf
SEQ ID NO:8	hiap2	..medstil	sdwtms.nkq
SEQ ID NO:44	consensus	..medstil	sdwtms.nkq

51	BIR 1	100
cp-iap	vangFFaTgk	wleaeChfch
diap	ARAGFLYTge	gdtVqCfSch
m-xiap	ARAGFLYTge	gdtVrcfSch
xiap	ARAGFYTTGv	ndkVkcfcCg
hiap1	ARAGFYTTGv	ndkVkcfcCg
hiap2	ARAGFYTTGv	ndkVkcfcCg
consensus	ARAGFYTTG-	-D-V-CF-C-

101	150
cp-iap	..feng
diap	..feng
m-xiap	..feng
xiap	..feng
hiap1	..feng
hiap2	..feng
consensus	..feng

Fig. 8 (page 1 of 5)

```

151
cp-iap .....MSD 1r1.....
diap esDnegnsvv .....dspeScsCPD 111.....
m-xiap ppeThady11 rtgqvVDiSD tiyprnp.am cSEEARLkSF qnWpdyahLt
xiap pSEthady11 rtgqvVDiSD tiyprnp.am ycEEARLkSF qnWpdyahLt
hiap1 ang.....Efsa 1mrssypcpM nEnARL1TF qtwP.1tfIs
hiap2 ave.....Diss strnpysyam stEEARF1TY hmWP.1tfIs
consensus --E-----D-SD -----M --EEARL-TF --WP----L-
200

```

BIR 2

```

201
cp-iap PetMAknGFY YIGrsDeVrC afCkveImrw kegeEdpaADH kKwApqCpFV
diap pgalakAGFY YInrIdhVkc wCnGviakw EkndAfeEH KRfFPqCpRV
m-xiap PRELASAGLY YtGadDqVqC FCCGgKlKlNW EPcDrAwSEH rRHFpncfFV
xiap PRELASAGLY YtGigDqVqC FCCGgKlKlNW EPcDrAwSEH rRHFpncfFV
hiap1 PtDLARAGFY YigPgDrVAc FACGgKlSNW EPkDnAmSEH 1RHFPKCPFI
hiap2 PSELARAGFY YigPgDrVAc FACGgKlSNW EPkDnAmSEH rRHFpncPFI
consensus P-ELA-AGFY Y-G--D-V-C F-CGgKl-NW EP-D-A-SEH -RHFP-CPFV
250

```

BIR 3

```

251
cp-iap kgIdvcgsiv ttniGnttt hdtIiGPahP kyAheaARvk sFhnWPrcmk
diap qmgplie.fa tGknldelgi qptt1.PlrP kYAcvDARlR TfTdWPisNI
m-xiap lgrnvvrse s.gvssdrnf pnstnsPrNP aMAeyearIv TFgtWiYS..
xiap lgrnlNrse sdavssdrnf pnstnlPrNP smAdyeARlF TFgtWiYS..
hiap1 .....enqlqdtSry tVS.....N1 smQtHaARfk TFInWPSSv1
hiap2 .....ensl.etlrf sis.....N1 smQtHaARmr TFmyWPSSvP
consensus -----F --S---P-NP -MA---AR--TF--WP-S--
300

```

Fig. 8 (page 2 of 5)

BIR 3

	301		350
cp-iap	qrpeQmAdAG	FFYtGyGdnt	KCFYCdGGLk
diap	qpasAlaQAG	LYYqkiGdq	rCFhCniGLr
m-xiap	VnKEQLARAG	FYAlGeGDkV	KCFhCgGGLt
xiap	VnKEQLARAG	FYAlGeGDkV	KCFhCgGGLt
hiap1	VnpeQLASAG	FYYVgnsDdv	KCFcCdGGLr
hiap2	VqpeQLASAG	FYYVGRSddv	KCFgcCdGGLr
consensus	V--EQLA-AG	FYY-G-GD-V	KCF-C-GGL-
			-W---DDPW-
			QHAKWFP-C-

	351		400
cp-iap	YVqLVKGRDY	VqkvIt
diap	FvllakGpay	VseVlatta	nassqpaTap
m-xiap	YlldeKQGEY	Innihlthp	leESlgrTae
xiap	YlldeKQGEY	Innihlthp	leESlgrTae
hiap1	YllirIKQGEY	Irqvqasyph	LlEqlLstSD
hiap2	FlirmKQGEF	VdeiqrYph	LlEqlLstSD
consensus	YL---KGQEX	-----	L-E-L--T--
			-----P-----

	401		450
cp-iap	..acVLpge.
diap	..adVLmdea	pakeAlTLGi	dggvVrnaig
m-xiap	kiDdtifqnP	mVgeAirmGF	sfkdlKktme
xiap	riDdtifqnP	mVgeAirmGF	sfkdlKktme
hiap1	seDaImntP	vlnaAveMGF	srsLVKqtvq
hiap2	seDaVmntP	vKsAlEmGF	nrdlVKqtvI
consensus	--D-V-----P	-V--A--MGF	-----VK-----
			-KI--G--Y
			-----LV-DL

Fig. 8 (page 3 of 5)

Ring Zinc Finger

	551		600
cp-iap	...tki....	qkmsvstpnq	..Ekepq
diap	sniskitdei	nlsleEenRq	vedsklckic
m-xiap	distEEQLR	Lkdarlckvc
xiap	k eisteEQLR	LqEEKlskic
hiap1	lyehlfvqgd	dkyiptedvs	LqEEKlckic
hiap2	lyknlfvdkn	mkypitedvs	LpEErtckvc
consensus	-----	-----	LqEErtckvc
			MDKEVSVFI
			MD-EV--VF-

	601		635
cp-iap	PCGHVvAcak	CAISvdKCPM	QRkiVtSVlk
diap	PCGHLatCnq	CAPsvancPM	QRadIkqfvr
m-xiap	PCGHLatCkq	CAeavdKCPM	QytVIttnqk
xiap	PCGHLVtCkq	CAeavdKCPM	QytVIttfkqk
hiap1	PCGHLVvCkd	CAPslrKCPi	QRstIkgtvr
hiap2	PCGHLVvCqe	CAPslrKCPi	QRgIlkgtvr
consensus	PCGHLV-C--	CA-SV-KCPM	QR--I-----
			-FLS-

Fig. 8 (sheet 5 of 5)

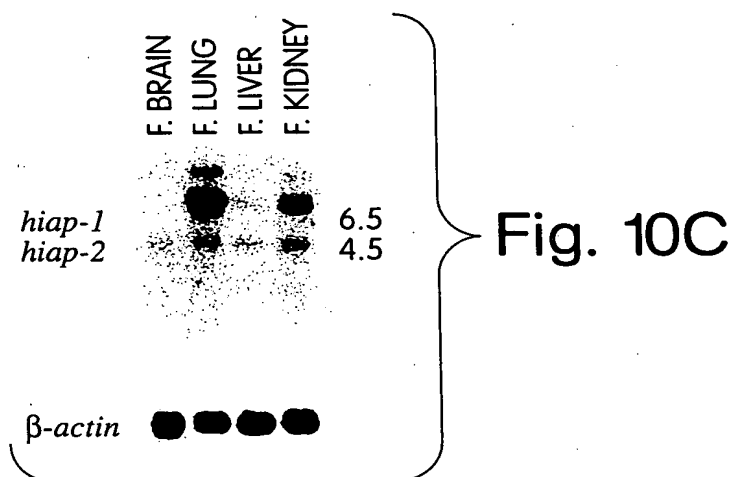
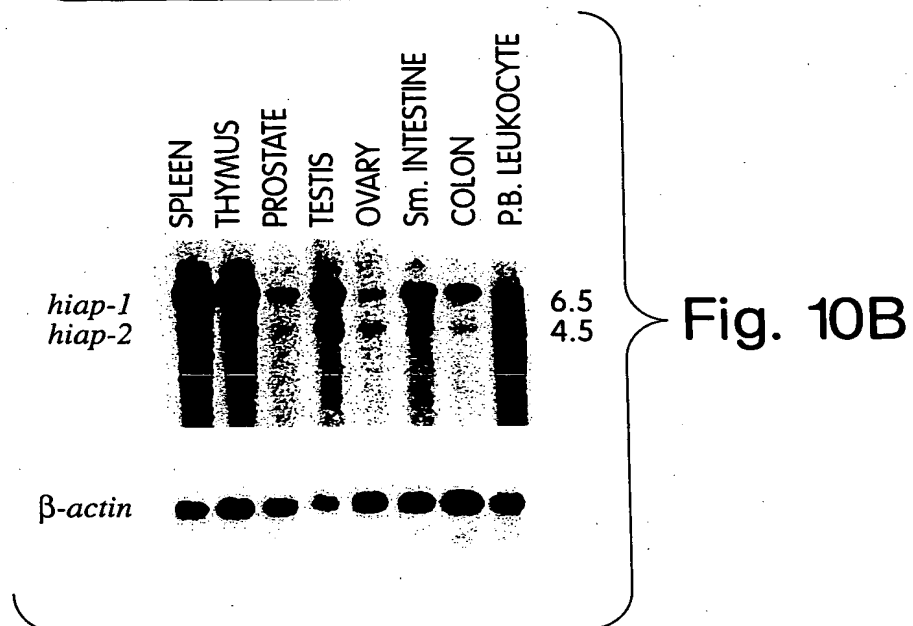
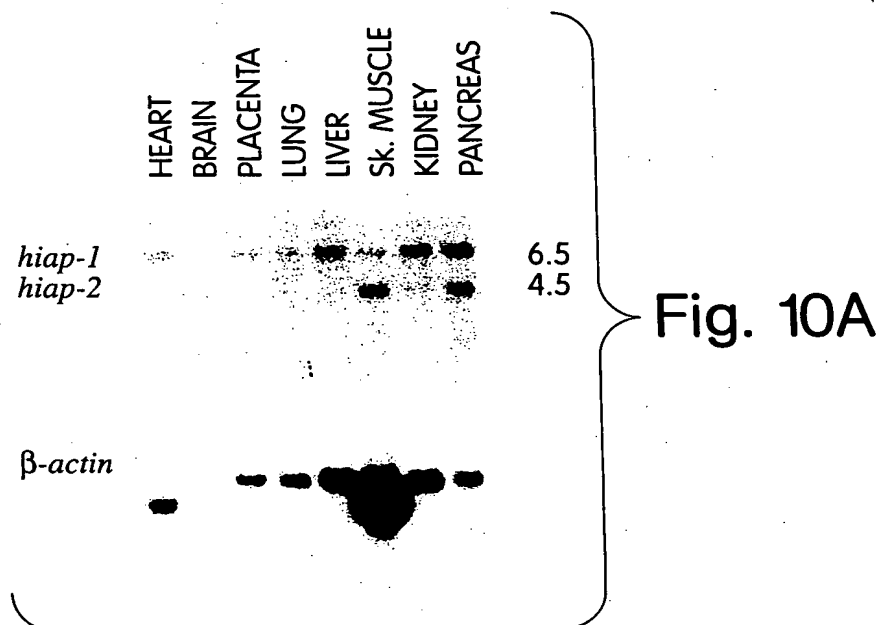
Alignment of RZF (Ring Zinc Finger) Domains

Baculovirus		
Cp_iap		Cydia pomonella
Op_iap		Orgyia pseudotsugata
Human		
xiap		IAP on X chromosome
hiap1, hiap2		two different human IAP genes
Mouse		
m-xiap		mouse homologue of human xiap gene
Insect		
diap		Drosophila IAP gene, not clearly a homologue of xiap or hiap

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

SEQ ID NO:32	hiap2	1	EqlrrlqEer	tCKVCMdkev	svvFIpCGHl	vvCqgeCApel	rkCPiC	46
SEQ ID NO:33	hiap1		EqlrrlpEer	tCKVCMdkev	sivFIpCGHl	w CKdCApsl	rkCPiC	
SEQ ID NO:34	m-xiap		EqlrrlqEek	lSKICMdrni	aivFFpCGHl	atCKqCAeav	dkCPmC	
SEQ ID NO:35	xiap		EqlrrlqEek	lCKICMdrni	aivFFpCGHl	vtCKqCAeav	dkCPmC	
SEQ ID NO:36	diap		EnrqldkDar	lCKVCLdeev	gvvFIpCGHl	atCnqCApev	ancPmC	
SEQ ID NO:37	Cp_iap		Ekepyvedsk	lCKICyveec	ivcFvPCGHv	vaCaKCAIsv	dkCPmC	
SEQ ID NO:38	Op_iap		aveaevAdDr	lCKIClqack	tvCFvPCGHv	vaCgkCAagv	ttCPvC	
SEQ ID NO:1	consensus		E-----E--	-CKICM----	-V-F-PCGH-	--C--CA---	--CP-C	

Fig. 9



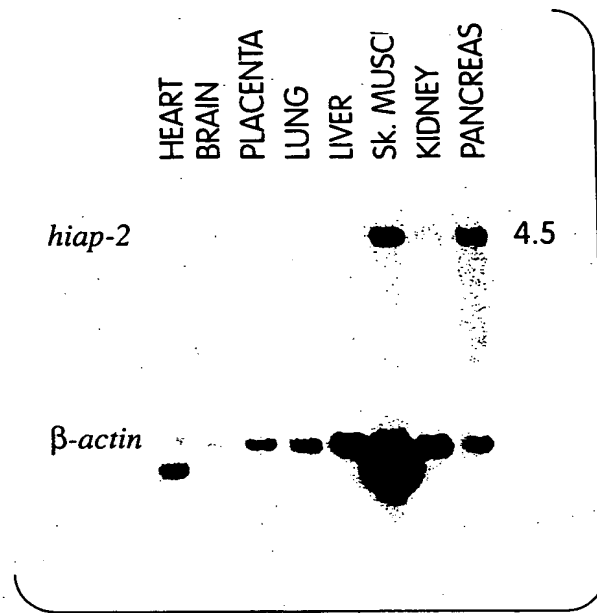


Fig. 11A

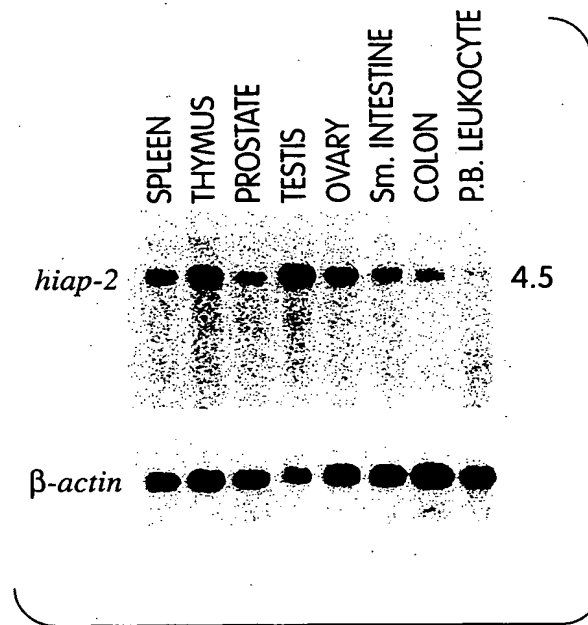


Fig. 11B

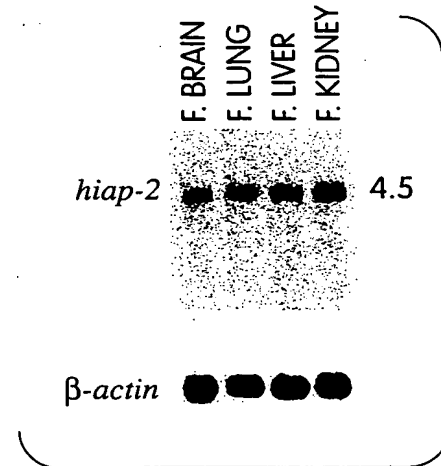


Fig. 11C

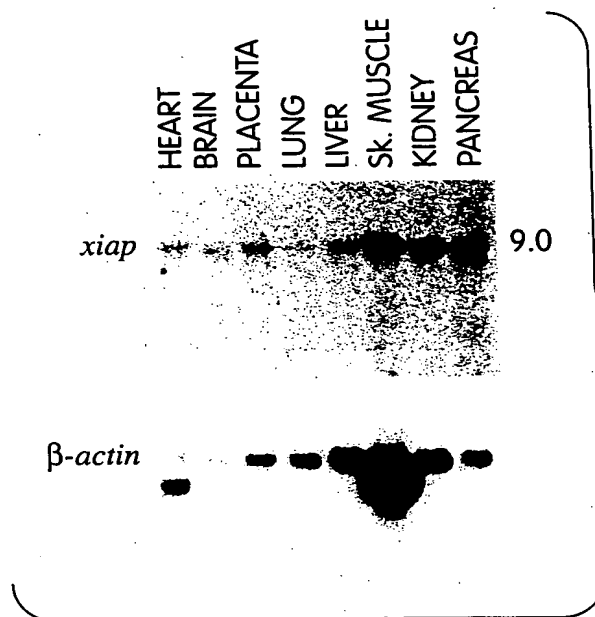


Fig. 12A

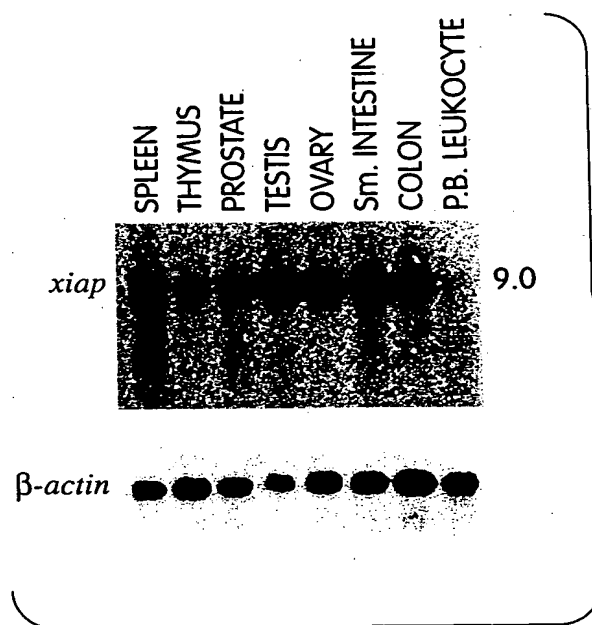


Fig. 12B

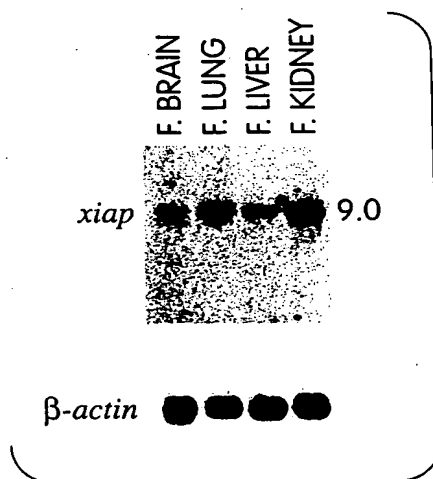


Fig. 12C

S: STANDARDS		INCUBATION: OVERNIGHT											
		Hg			CEM-CM ₃			GT/CEM			JKT		
HIV		-	-	+	-	-	+	-	-	+	-	-	+
PHA/PMA		-	+	-	-	+	-	-	+	-	-	+	-
S		+	-	-	+	-	-	+	-	-	+	-	-

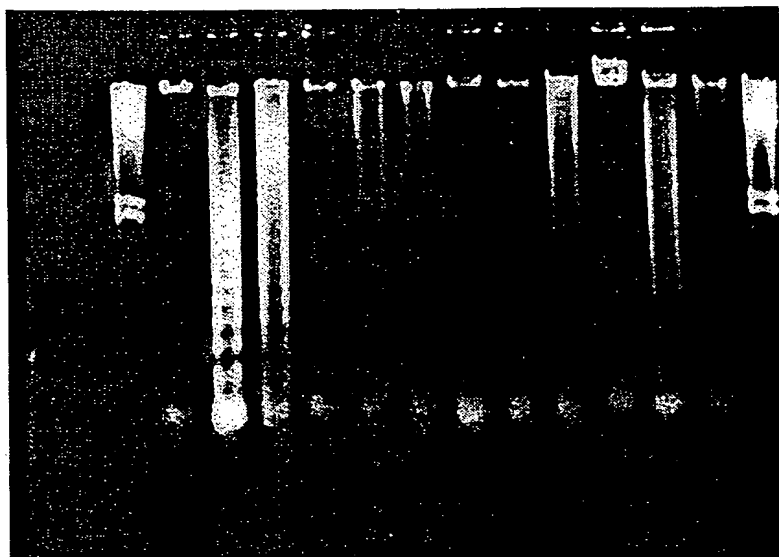


Fig. 13A

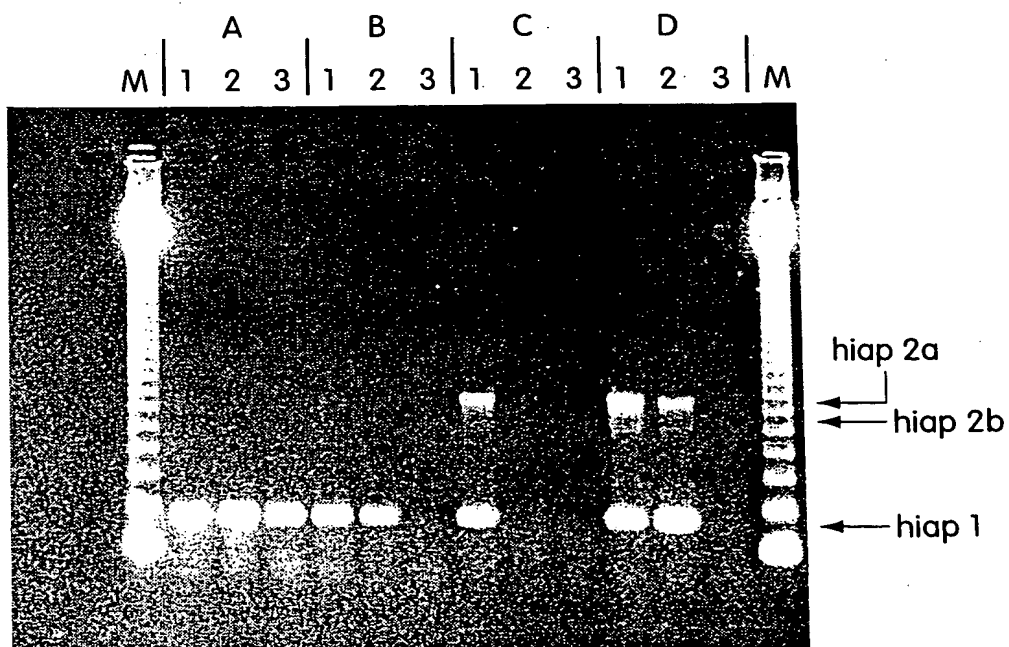


Fig. 13B

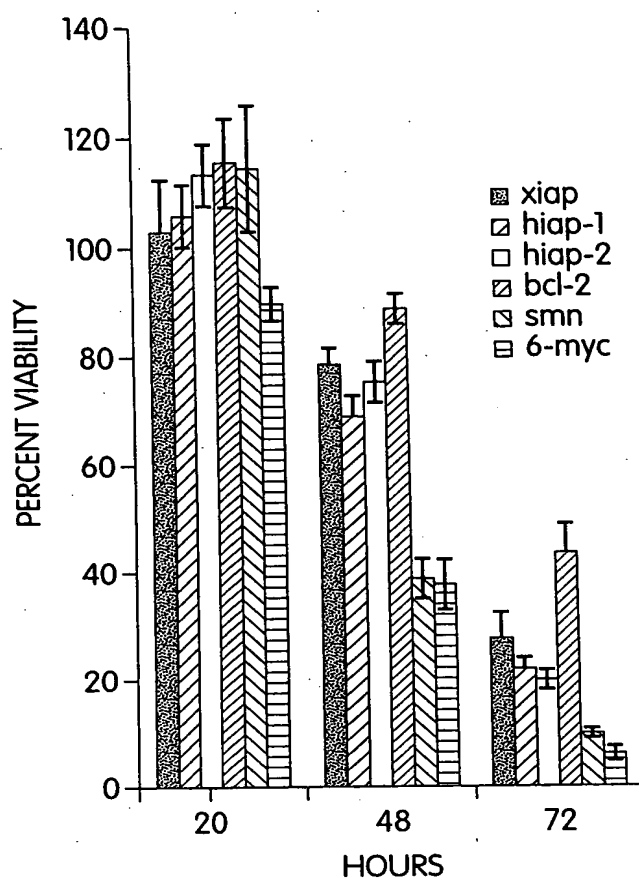


Fig. 14A

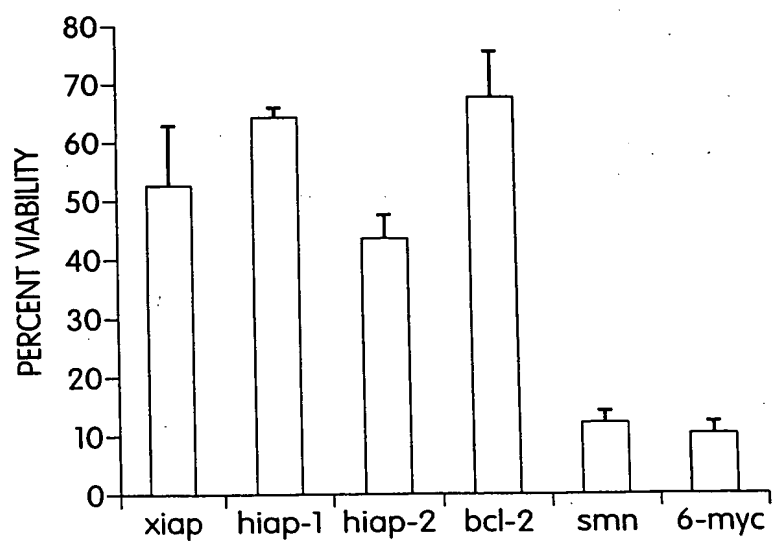


Fig. 14B

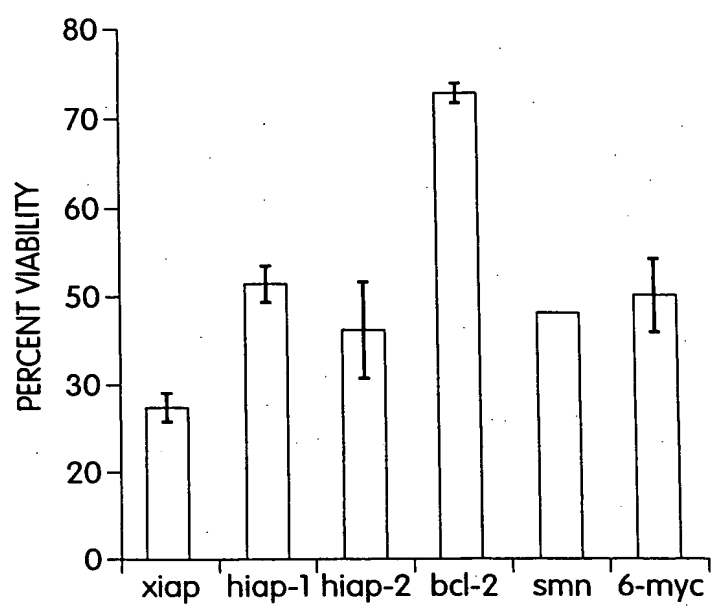


Fig. 14C

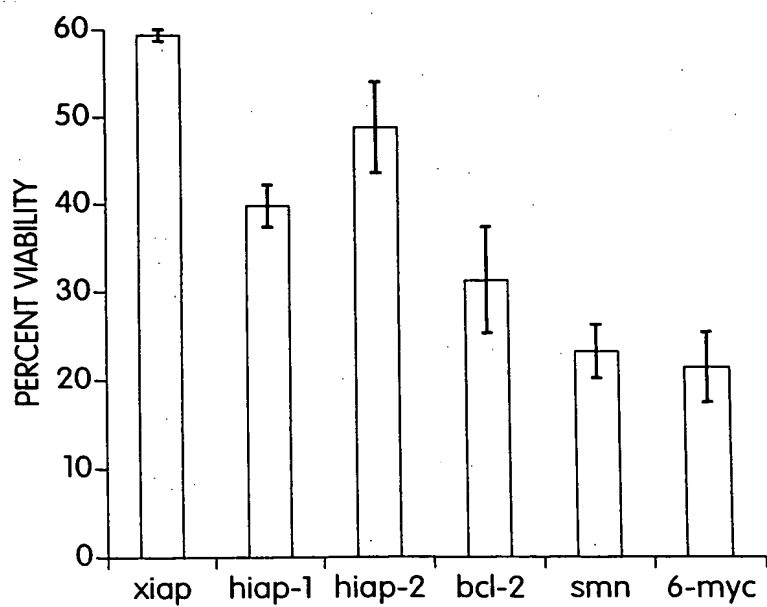


Fig. 14D